

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 15:40:09 ON 06 APR 2001
L1 406 SEA PLU=ON (TRANSGENIC) AND (PLANT OR TOBACCO OR BARLEY OR
RICE OR BRASSICA OR PICEA OR SOYBEAN) AND (DIGEST?)
D KWIC

L2 258 SEA PLU=ON L1 NOT PY>1998
L3 172 DUP REM L2 (86 DUPLICATES REMOVED)
D KWIC

L4 19 SEA PLU=ON L3 AND (DIGEST?)/TI
D TI 1-19
D IBIB AB 4

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 15:46:35 ON 06 APR 2001
L5 97 SEA PLU=ON (TRANSGENIC) AND (PLANT OR TOBACCO OR BARLEY OR
RICE OR BRASSICA OR PICEA OR SOYBEAN) AND (ALLERGEN?)
L6 61 SEA PLU=ON L5 NOT PY>1998
L7 36 SEA PLU=ON L6 AND ALLERGEN?/TI
L8 30 DUP REM L7 (6 DUPLICATES REMOVED)
D TI 1-30

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 15:52:18 ON 06 APR 2001
L10 2 SEA PLU=ON L9
D TI 1-2
D IBIB AB 1-2

L11 6052 SEA PLU=ON THIOREDOXIN
L12 142 SEA PLU=ON THIOREDOXIN H
L13 13 SEA PLU=ON L12 AND (TRANSGENIC)
L14 8 DUP REM L13 (5 DUPLICATES REMOVED)
D TI 1-8
D IBIB AB 1-8

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 16:01:29 ON 06 APR 2001
L16 0 SEA PLU=ON L15
L17 8 SEA PLU=ON (TRXH? OR THIOH?) AND (TRANSGENIC)
L18 3 SEA PLU=ON L17 NOT L13
L19 3 DUP REM L18 (0 DUPLICATES REMOVED)
D IBIB AB 1-3
D IBIB AB 1-3

L20 50 SEA PLU=ON (THIOREDOXIN) AND (EXPRESS? OR TRANSFORM? OR
INTRODUCE?) (3A) (PLANT OR TOBACCO OR RICE OR BARLEY OR MAIZE
OR
WHEAT OR RYE OR SORGHUM OR MILLET OR TRITICALE OR FORAGE)
L21 44 SEA PLU=ON L20 NOT (L13)
L22 26 SEA PLU=ON L21 NOT PY>1998
L23 17 DUP REM L22 (9 DUPLICATES REMOVED)
L24 4 SEA PLU=ON L23 AND (THIOREDOXIN H)
L25 0 SEA PLU=ON L23 AND (THIOH? OR TRXH?)
L26 4 DUP REM L24 (0 DUPLICATES REMOVED)
D IBIB AB 1-4

Chau

(FILE 'HOME' ENTERED AT 17:06:32 ON 06 APR 2001)

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 17:06:42 ON 06 APR 2001
L1 0 S TRANSGENIC AND (PLANT OR RICE OR BARLEY OR TOBACCO OR MAIZE
O
L2 13 S TRANSGENIC AND (PLANT OR RICE OR BARLEY OR TOBACCO OR MAIZE
O
L3 11 DUP REM L2 (2 DUPLICATES REMOVED)

FILE

L Number	Hits	Search Text	DB	Time stamp
1	127	(transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticale forage) and (allergen\$6) (allergen\$6 near5 (reduc\$4 alter\$3 decreas\$3))	USPAT	2001/04/06 16:41
2	368	((allergen\$6 near5 (reduc\$4 alter\$3 decreas\$3))) and ((transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticale forage) and (allergen\$6))	USPAT	2001/04/06 16:22
3	15	(transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticale forage) and (earl\$3 near3 (germinat\$3 amylase))	USPAT	2001/04/06 16:44
4	33	(transgenic) and (plant tobacco rice barley maize wheat rye sorghum millet triticale forage) and (earl\$3 near3 (pullulanase amylase))	USPAT	2001/04/06 16:54
5	22	((transgenic) same pullulanase) and (plant tobacco rice barley maize wheat rye sorghum millet triticale forage)	USPAT	2001/04/06 17:04
6	0		USPAT	2001/04/06 17:05

L1 ANSWER 13 OF 14 AGRICOLA
ACCESSION NUMBER: 93:34770 AGRICOLA
DOCUMENT NUMBER: IND93018147
TITLE: Specific reduction of wheat storage proteins by thioredoxin h.
AUTHOR(S): Kobrehel, K.; Wong, J.H.; Balogh, A.; Kiss, F.; Yee, B.C.; Buchanan, B.B.
CORPORATE SOURCE: INRA, Montpellier, France
AVAILABILITY: DNAL (450 P692)
SOURCE: Plant physiology, July 1992. Vol. 99, No. 3. p. 919-924
Publisher: Rockville, Md. : American Society of Plant Physiologists.
CODEN: PLPHAY; ISSN: 0032-0889
NOTE: Includes references.
DOCUMENT TYPE: Article
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English
AB Gliadins and glutenins, the major storage proteins of wheat endosperm (*Triticum durum*, Desf. cv Monroe), were reduced *in vitro* by the NADP/thioredoxin system (NADPH, NADP-thioredoxin reductase and thioredoxin; in plants, the h type) from either the same source or the bacterium *Escherichia coli*. A more limited reduction of certain members of these protein groups was achieved with the reduced form of glutathione or glutaredoxin, a protein known to replace thioredoxin in certain bacterial and mammalian enzyme systems but not known to occur in higher plants. Endosperm extracts contained the enzymes necessary to reduce NADP by the oxidative pentose phosphate pathway (hexokinase, glucosephosphate 6-dehydrogenase, 6-phosphogluconate dehydrogenase). The gliadins and glutenins were also reduced *in vivo* during germination--an event that accompanied their proteolytic breakdown. The results suggest that thioredoxin, reduced by NADPH generated via the oxidative pentose phosphate pathway, functions as a signal in germination to enhance metabolic processes such as the mobilization of storage proteins and, as found earlier, the activation of enzymes.

HITS AT: 37-75

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L11 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2002 ACS

RN 163539-45-5 REGISTRY

CN DNA (barley clone Hor3-1 gene Hor3 fragment plus 5'-flank) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (barley clone Hor3-1 gene Hor3 fragment plus 5'-flanking region fragment)

OTHER NAMES:

CN GenBank X84368

FS NUCLEIC ACID SEQUENCE

SQL 1859

NA 548 a 550 c 462 g 299 t

NTE doublestranded

SEQ 1 cttcgagtgc ccggcgattt gccagcaatg gctaacagac acatattctg
51 cccaaacccc agaacaataa tcacttctcg tagatgaaga gaacagacca
101 agatacaaac gtccacgcct cagcaaaacag taccccgaaa ctaggattaa
151 gccgattacg cggttttagc agaccgtcca aaaaaactgt tttgcaaagc
201 tccaaattcct ccttgcttat ccaatttctt ttgtgttggc aaactgcact
251 tgtccaaaccg attttgttct tccctgtttt cttcttaggc taactaacad
301 agccgtgcac atagccatgg tccggaatct tcacctcgac cctataaaag
351 cccagccaat ctccacaatc tcatcatcac cgagaacacc gagaaccaca
401 aaactagaga tcaattcatt gacagtccac cggagatggct aagcggctgg
===== =====
451 tcctctttgt ggcggtaatc gtcgcccctcg tggctctcac caccgctgaa
===== =====
501 cgtgagatca atggaaacaa cattttcctt gatagccgct ctaggcagct
551 acagtgtgag cgccgagctcc aggagagctc gtcgaggcg tgccggcggg
601 tcgtggacca acagctgtt ggccagctgc catggagcac ggggctccag
651 atgcagtgtc gccagcgtc tcgggacgtc agccccgagt gcccggccgt
701 cgcctcagc caggtcgatc ggcaatacga gcagcaaacc gaggtgccat
751 ccaagggagg atccttctac ccgggcggga ccgcaccgccc gctgcagcaa
801 ggaggatggt gggaaacctc tgtaaaatgg aactaccag accaaacctc
851 ttcgcaacag tcatggcaag ggcaacaagg gtaccacaa agcgttaactt
901 cttcccagca gccaggacaa gggcagcaag ggtcctaccc aggttcaact
951 ttcccgacg agccaggaca aggacaacaa ccaggacaga ggcagccatg
1001 gtcctatcca agtgcacatt tccacaaca gccaggcga gggcaaggc
1051 aacaagggtt ctacccaggc gcaacttccc tgctgcagcc aggacaagg
1101 caacaagggc cctaccagag tgcaacttct ccacagcagc cagacaagg
1151 acagggacaa caagagacct atccaattgc aacttccccg catcagccag
1201 gacaatggca acaaccagga caagggcaac aagggtacta cccaaatgt
1251 acttctccac aacagtcggg acaaggcga caagggtacc caagtacaac
1301 ttctccacaa caatcgggc aaggcaaca gctggacaa gggcaacaac
1351 caggacaagg gcaacaaggg taccgaatgt caactttcc acaacagcca
1401 ggacaatggc aacaagggtc ctacccaagt acaacttctc cgcagcagtc
1451 aggacaaggg caacaagggt acaacccaag tggaaacttct acgcagcagt
1501 cgggacaagt gcatcagttg ggacaaggc aacaaggta ctacccaatt
1551 gcaacttctc cgcagcagcc aggacaaggg caacagctag gacaaggcga

1601 acaaccagga catgggcaac agcttagtgca agggcaacaa caaggacaag
1651 ggcaacaagg acactaccca agtatgactt ctccgcacca aacaggacaa
1701 gggcaaaaag gatactaccc aagtgcatt tctccgcagc agtcaggaca
1751 aggacaacaa ggataccgc ctagtggagc ttcttcacag gggtcgggtgc
1801 aaggggcggtg ccagcacagc acatcttctc cgcagcagca agcacaaggg
1851 tgccaagct

HITS AT: 435-473

MF Unspecified

CI MAN

SR GenBank

LC STN Files: AGRICOLA, CA, CAPLUS, GENBANK

1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

L11 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2002 ACS
RN 172866-15-8 REGISTRY
CN DNA (barley D hordein gene promoter region-containing fragment) (9CI)
(CA
INDEX NAME)
FS NUCLEIC ACID SEQUENCE
SQL 2296
NA 629 a 708 c 606 g 353 t

SEQ 1 caaaaactaga gatcaattca ttgacagtcc accgagatgg ctaagcggct
===== =====
51 ggtcctcttt gtggcggtaa tcgtcgccct cgtggctctc accaccgctg
===== =====
101 aacgtgagat caatggaaac aacatttcc ttgatagccg ctctaggcag
151 ctacagtgtg agcgcgagct ccaggagagc tcgctcgagg cgtgcccggcg
201 ggtcgtggac caacagctgg ttgccagct gccatggagc acggggctcc
251 agatcgatg ctgccagcag cttcgggacg tcagccccga gtggccggcccc
301 gtcgccccta gccaggtcg gaggcaatac gagcagcaaa ccgagggtgcc
351 atccaaggga ggatccttcc accccggcg gaccgcaccc ccgctgcagc
401 aaggaggatg gtggggacc tctgtaaaat ggtactaccc agaccaaact
451 tcttcgcaac agtcatgca aggcaacaa gggtaaccacc aaagcgtaac
501 ttcttcccag cagccaggac aaggcagca agggtcctac ccaggttcaa
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601 tggtcctatc caagtgcac tttcccacaa cagccagggc aaggggcaagg
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701 ggcaacaagg gccctaccag agtgcacatt ctccacagca gccaggacaa
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851 taacttctcc acaacagtgc ggacaagggc aacaagggtt cccaaagtaca
901 acttctccac aacaatcggg gcaaggggca cagctgggac aaggggcaaca
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2001 tggtcagcag tccaaacgatgtactacgg cagccatac catgttagcg
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2101 ggcgcagctgc cggcaatgtg tcggctggag ggcggccggc gcctgttggc
2151 cagccagtag tagaactctg gcagctcgca tggtgcttgg gcatgc
2201 accttagcta tacaataaac gtgacgtgtg cttgcagttt ttcatgtaac
2251 taggtaaaa cccaaacaata atgcaaaaacg gaaagtttccatcc

5 ANSWER 6 OF 9 AGRICOLA
ACCESSION NUMBER: 1998:12132 AGRICOLA
DOCUMENT NUMBER: IND20615782
TITLE: Self-incompatibility in the grasses: evolutionary relationship of the S gene from Phalaris coerulescens to homologous sequences in other grasses.
AUTHOR(S): Li, X.; Paech, N.; Nield, J.; Hayman, D.; Langridge, P.
CORPORATE SOURCE: University of Adelaide, Glen Osmond.
SOURCE: Plant molecular biology, May 1997. Vol. 34, No. 2. p. 223-232
NOTE: Includes references
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Article
FILE SEGMENT: Non-U.S. Imprint other than FAO
LANGUAGE: English
AB Self-incompatibility is widespread in the grasses and it is proposed that the grasses share a common incompatibility mechanism that is distinct from those operating in the dicotyledonous species studied in great detail. Where good genetic data are available, all grass species appear to have an incompatibility mechanism controlled by two unlinked loci, S and Z. A putative S gene has been cloned from Phalaris coerulescens. This gene is characterized by two major domains: an allele specificity domain and a thioredoxin catalytic domain. A family of sequences with varying degrees of homology to this gene has been identified among 15 grass species covering all subfamilies of the Poaceae. These S-related sequences appear to be present in the grass family regardless of self-compatibility. Evidence is presented to show that at least one of the sequences is transcribed, suggesting a functional gene. In contrast to the high expression of the S gene in Phalaris pollen, expression of the related gene in the pollen (or anthers) of the grass species examined was so low that RNA gel blot analysis failed to display a significant signal. However, reverse transcription-based polymerase chain reaction (RT-PCR) successfully amplified the region corresponding to the S thioredoxin domain from 10 of the grass species. With grasses other than Phalaris, RT-PCR showed limited success in amplifying the region corresponding to the S variable portion at the 5' end of the Phalaris S gene. Sequencing of the PCR-amplified S thioredoxin region from wheat, barley, rye and Dactylis revealed that this is a highly conserved gene with 94-97% sequence similarity with the corresponding Phalaris S gene. The conservation of sequence and ubiquitous expression of the gene across the grass family strongly suggest that the S-related gene is carrying out a significant biological function in the Poaceae. On the basis of these findings, a model for the evolution of the S self-incompatibility gene in the grasses is proposed.

DUPPLICATE 3